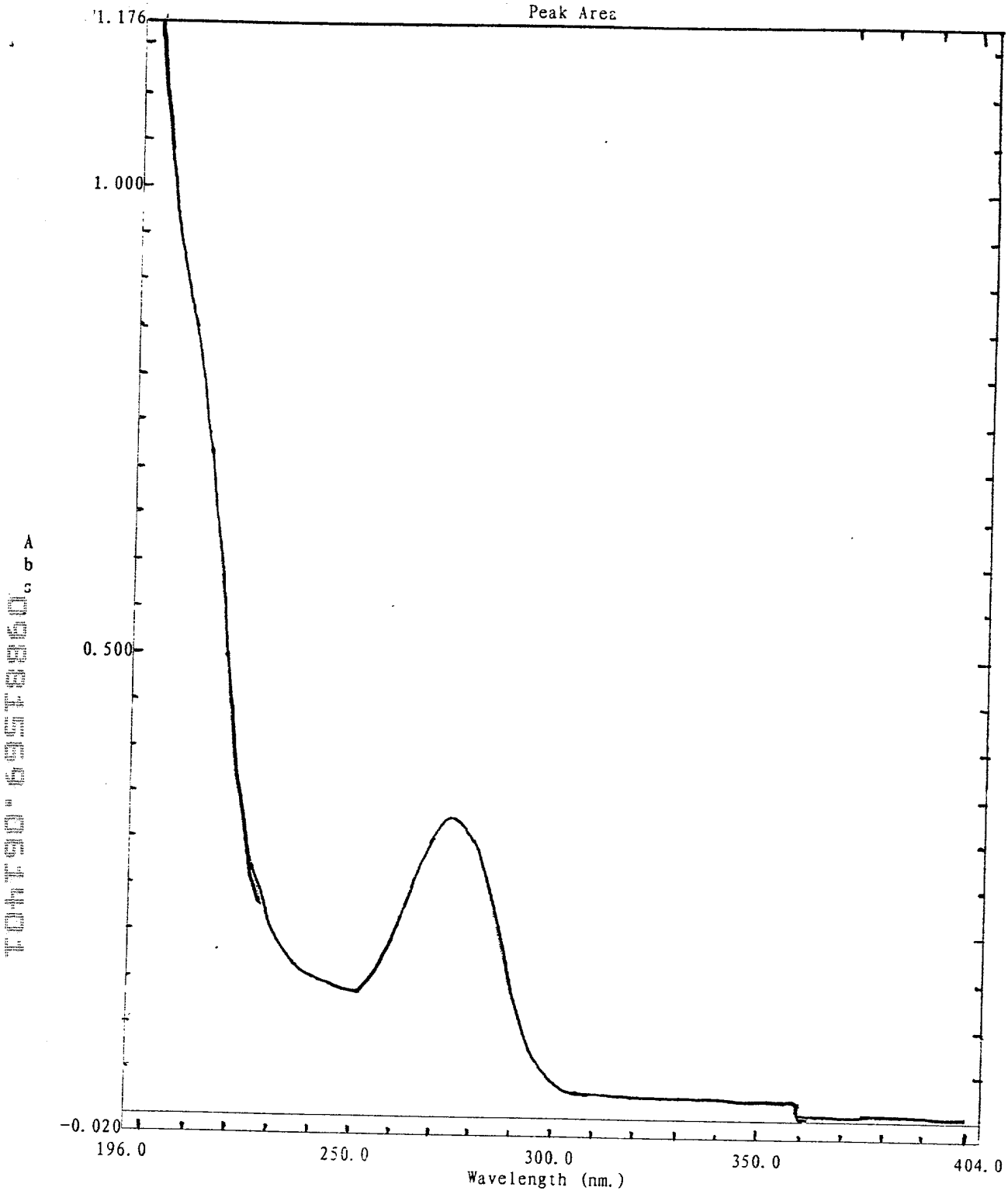


File Name: SY-12

Created: 14:29 01-01-22
Data: Original

Measuring Mode: Abs.
Scan Speed: Fast
Slit Width: 1.0
Sampling Interval: 0.2

FIG.1

Result = (Area • Factor) / Divisor Factor = 0.000

Region	Start	End	Divisor	Area	Result

CAMAG TLC Evaluation Software

ARBRO PHARMACEUTICALS LTD 6/14 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI
PHONE:5467228,515-0437,FAX 91 11-5460784,E-mail arbro@vsnl.com

TLC/HPTLC-Integration (CATS3.18 S/N:0207A001 / SCANNER II V3.14 S/N:990602)

ESTIMATION OF L-LYSINE BY HPTLC

Calibr.Table	Calibration table, created : ARBRO PHARMA LTD	
	File name : AMINO	3/JUN/ 0 14:49:46
Scan	User name while measuring : ARBRO PHARMA LTD	
	File name : AMINO	3/JUN/ 0 14:54:52
Integration	User while integrating : ARBRO PHARMA LTD	
	File name : AMINO	3/JUN/ 0 15:19:25

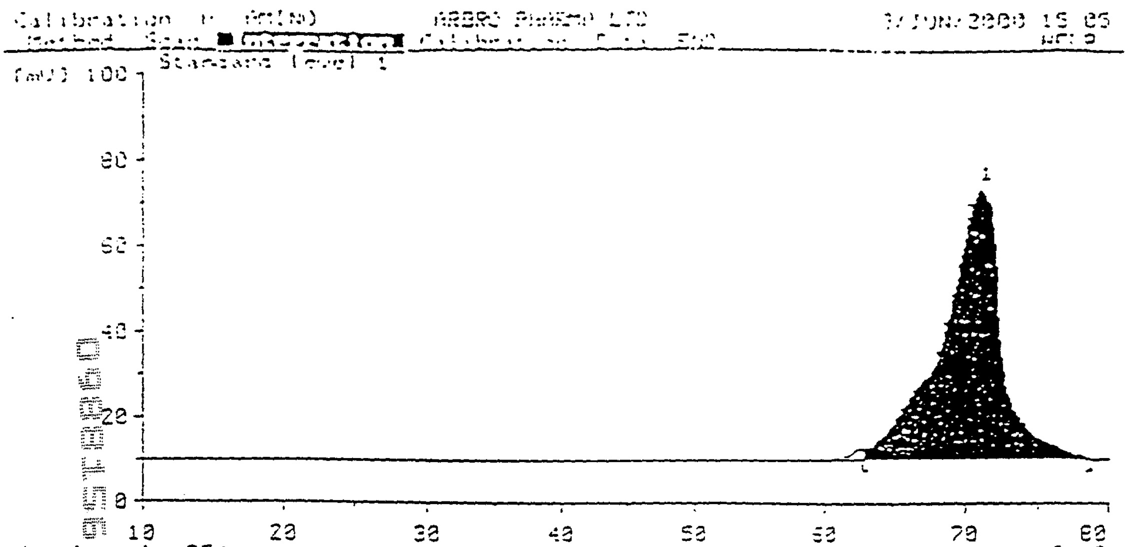
Track 1. Analysis a:

Peak #	start mm	start h	max mm	max h	max [%]	end mm	end h	area a	area [%]
1	61.1	0.4	72.6	64.1	100.00	79.2	0.1	3186.2	100.00
	Total height =		64.1			Total area =		3186.2	

Track 2. Standard level 1

Peak #	start mm	start h	max mm	max h	max [%]	end mm	end h	area a	area [%]
1	62.9	2.8	71.0	63.5	100.00	79.9	0.0	3133.9	100.00
	Total height =		63.5			Total area =		3133.9	

FIG.2(a)



Wavelength: 254 nm
Track: 2, noise level: 0.100mU, raw data file: AMINO
CATS3.10 S/N:0227A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 992502

rack 2. Standard level 1

eak	start		max			end		area	
#	mm	h	mm	h	[%]	mm	h	a	[%]
1	62.9	2.8	71.0	63.5	100.00	79.8	1.0	3133.9	100.00

Total height = 63.5 Total area = 3133.9

FIG.2(b)

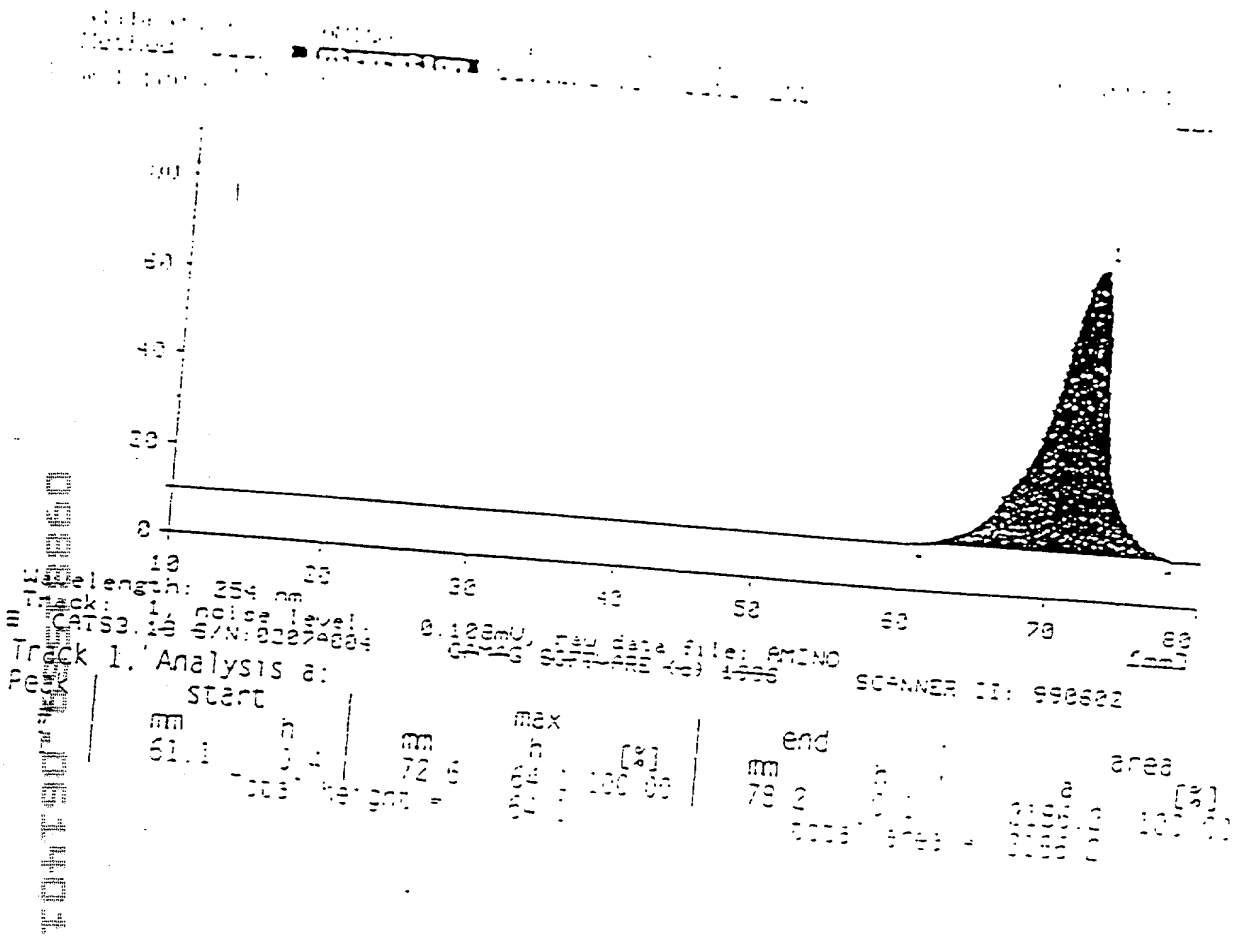

60
40
20
0
10
30
40
50
60
70
80
[cm]
Wavelength: 254 nm
Track: 1; noise level: 0.188mV, raw data file: AMINO
CATSA.16 S/N:0287e004
SCANNER II: 990602
Track 1, Analysis a:
Peak
Start
mm
61.1
max
mm
72.6
[%]
100.00
end
mm
79.2
area
[%]

FIG.2(c)

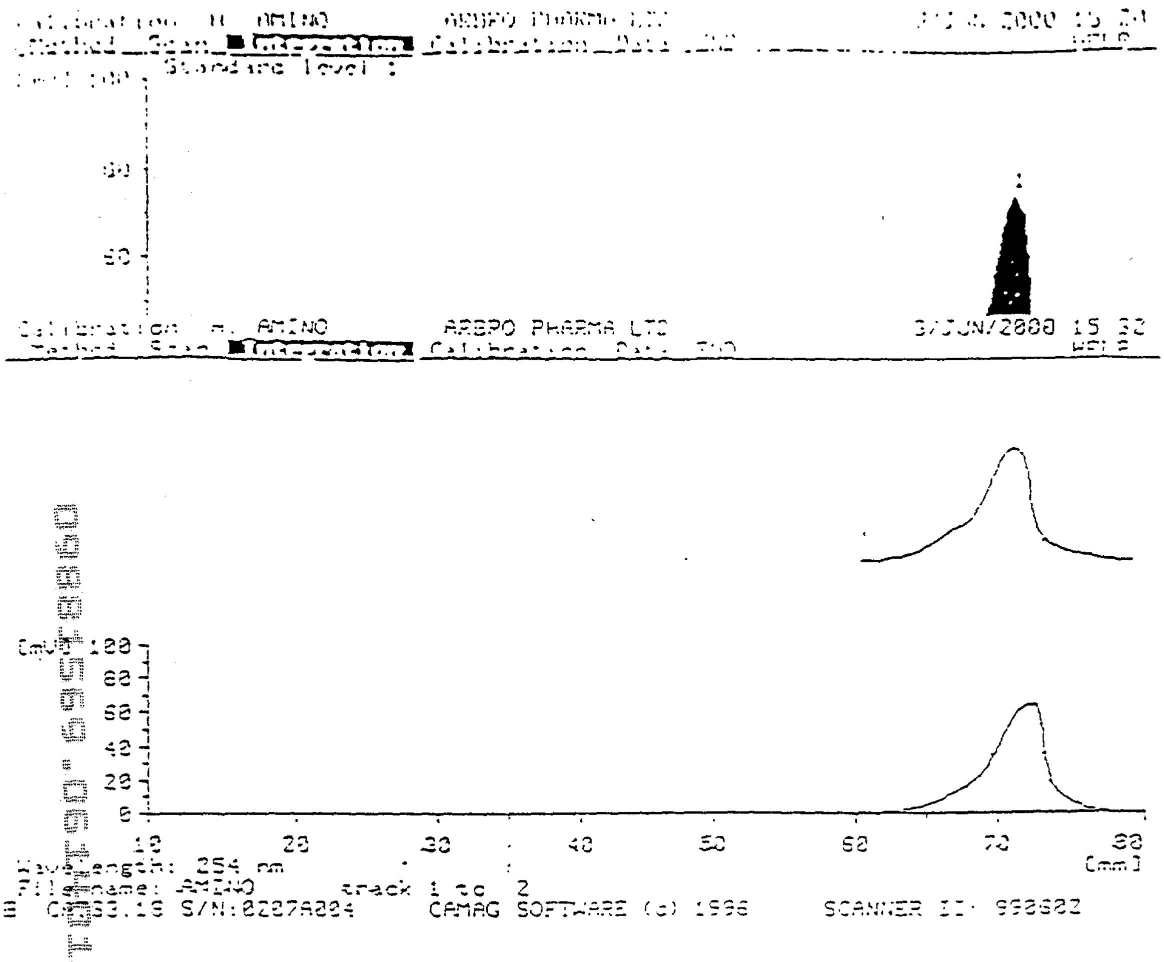


FIG.2(d)

SUBMITTER : PUSHPA KHANNA

SAMPLE NAME : GOURDIN DATE :

SEQUENCE :	ASP	LEU VAL	SER	GLN	GLN	TYR VAL	GLY	SER GLN THR	HIS ARG GLN LEU
CYCLE #:	1	2	3	4	5	6	7	8	9

SEQUENCE :	LYS ARG	TYR ILE LEU	ARG HIS ALA LYS	HIS GLU TYR	ASN ASP	ARG MET ILE	GLY ASP ASN LEU	ARG THR ASP	ARG HIS ALA
CYCLE #:	10	11	12	13	14	15	16	17	18

SEQUENCE :	SER GLU LEU LYS	ARG GLU	SER PRO ALA	ILE ASP	GLU LEU ILE	PHE TYR	THR SER ASN	PRO ARG ALA HIS	HIS ARG GLY
CYCLE #:	19	20	21	22	23	24	25	26	27

SEQUENCE :	GLY VAL ALA	GLY	ARG	VAL LEU ILE	ASN SER	PRO ILE THR	ALA VAL	ASN
CYCLE #:	28	29	30	31	32	33	34	35

YIELD (pmol) : ILE(2) 98.11 YIELD(pmol): GLU(3) 56.13

CARRYOVER : ILE(6) 22.6% REP YIELD: ILE(2,23) 92.3%

SEQSTD YIELD : NL(6) 2.30 SEQSTD CARRYOVER : NL(6) 23.0%

SEQSTD REP YIELD NL(6,11) 97.0%

COMMENTS : Mixtures with interchangeable amino acids at positions 12, 13, 15-19, 25-27 and 31-34. Appears to be a mixture of sequences.

FIG.3(a)

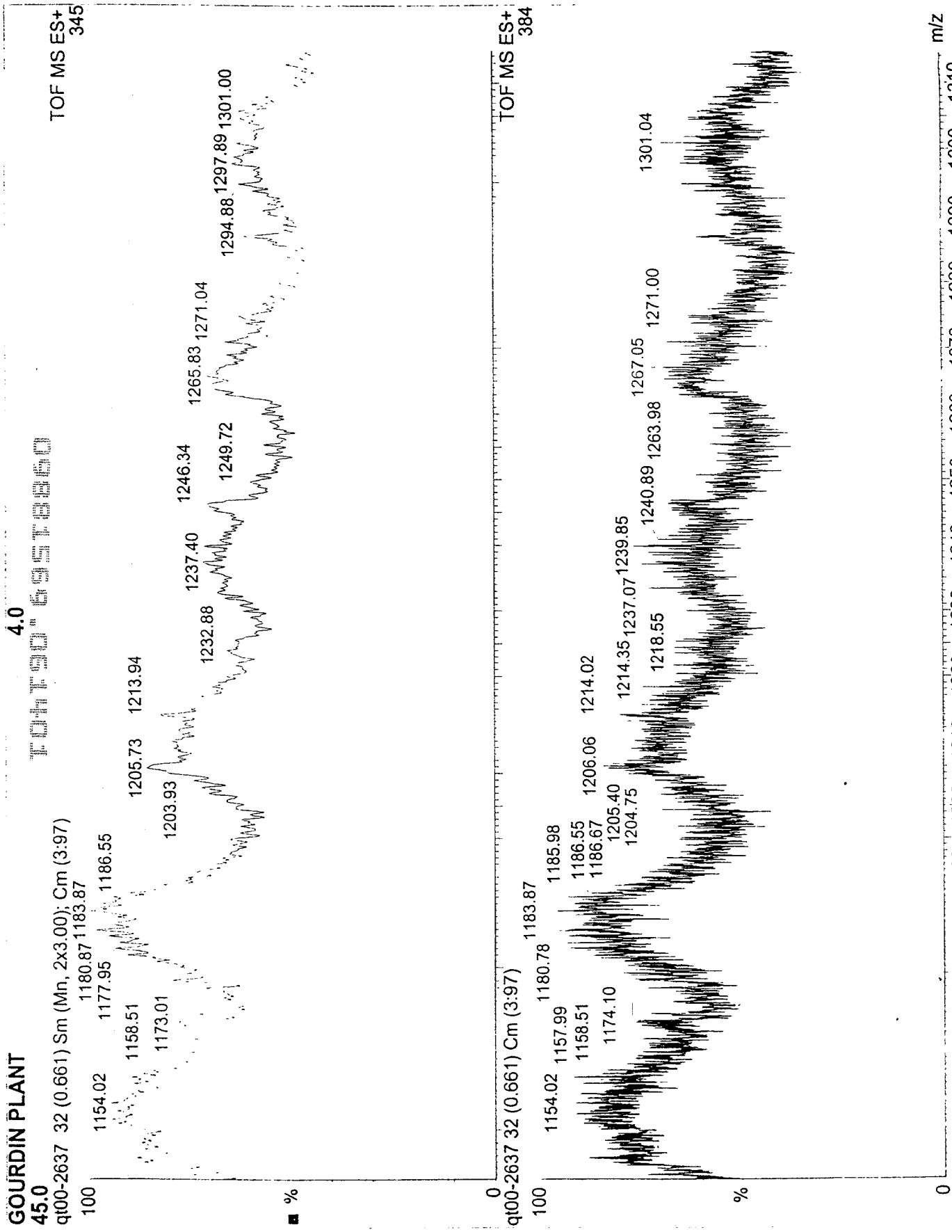

GOURDIN PLANT
4.0
45.0
qt00-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)
TOF MS ES+
345
100
%
0
1154.02
1158.51
1173.01
1177.95
1180.87
1183.87
1186.55
1203.93
1205.73
1213.94
1232.88
1237.40
1246.34
1249.72
1265.83
1271.04
1294.88
1297.89
1301.00
qt00-2637 32 (0.661) Cm (3:97)
TOF MS ES+
384
1154.02
1157.99
1158.51
1174.10
1180.78
1183.87
1185.98
1186.55
1186.67
1205.40
1204.75
1206.06
1214.02
1214.35
1218.55
1237.07
1239.85
1240.89
1263.98
1267.05
1271.00
1301.04
m/z
1150
1160
1170
1180
1190
1200
1210
1220
1230
1240
1250
1260
1270
1280
1290
1300
1310

FIG.4(a)

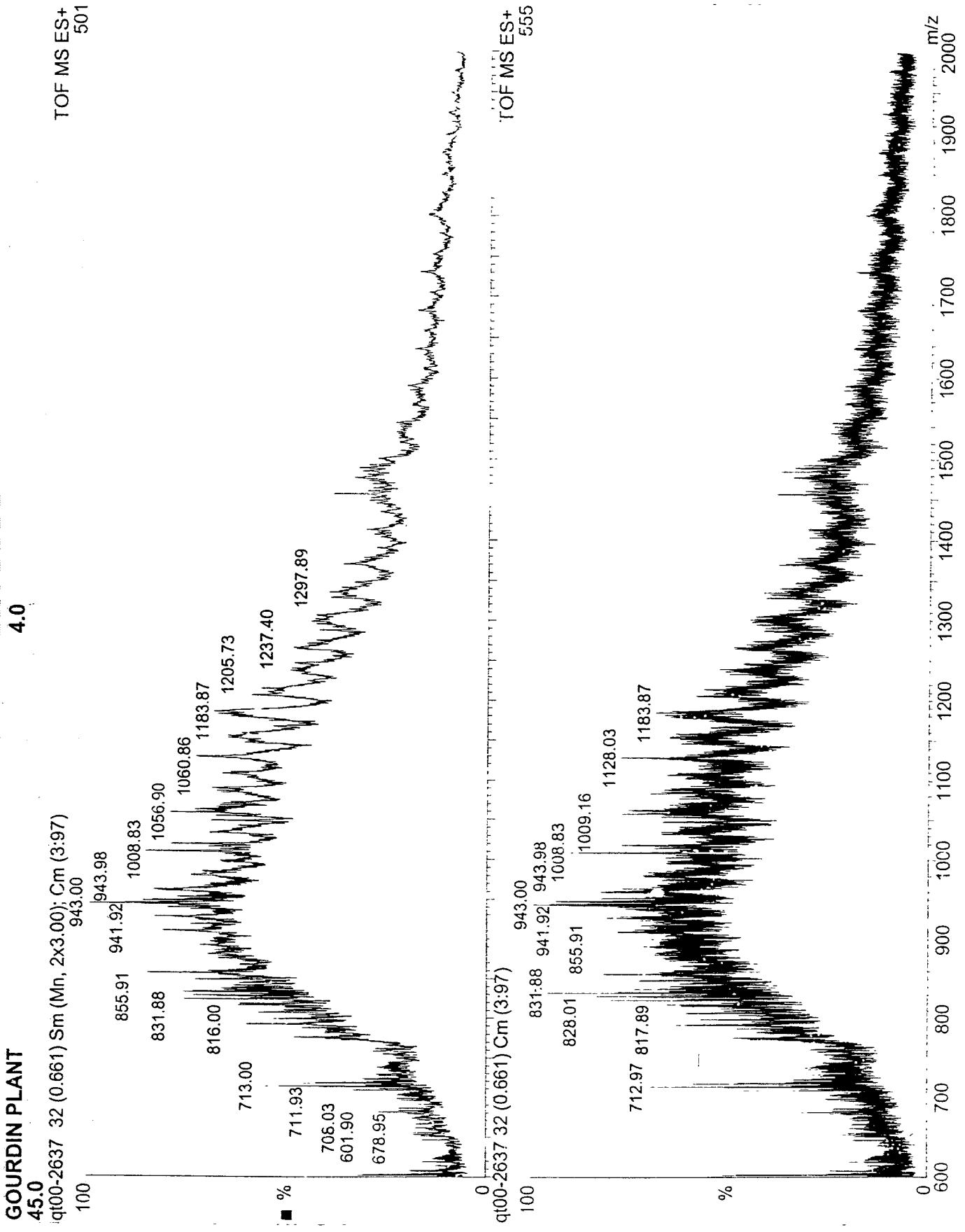

GOURDIN PLANT
45.0
4.0
qt00-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)
TOF MS ES+
501
943.00
943.98
941.92
855.91
1008.83
831.88
1056.90
816.00
1060.86
1183.87
713.00
1205.73
711.93
1237.40
706.03
601.90
1297.89
678.95
qt00-2637 32 (0.661) Cm (3:97)
TOF MS ES+
555
943.00
943.98
941.92
1008.83
831.88
855.91
1009.16
828.01
1128.03
712.97
817.89
1183.87
100
0
%
600
700
800
900
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z

FIG.4(b)

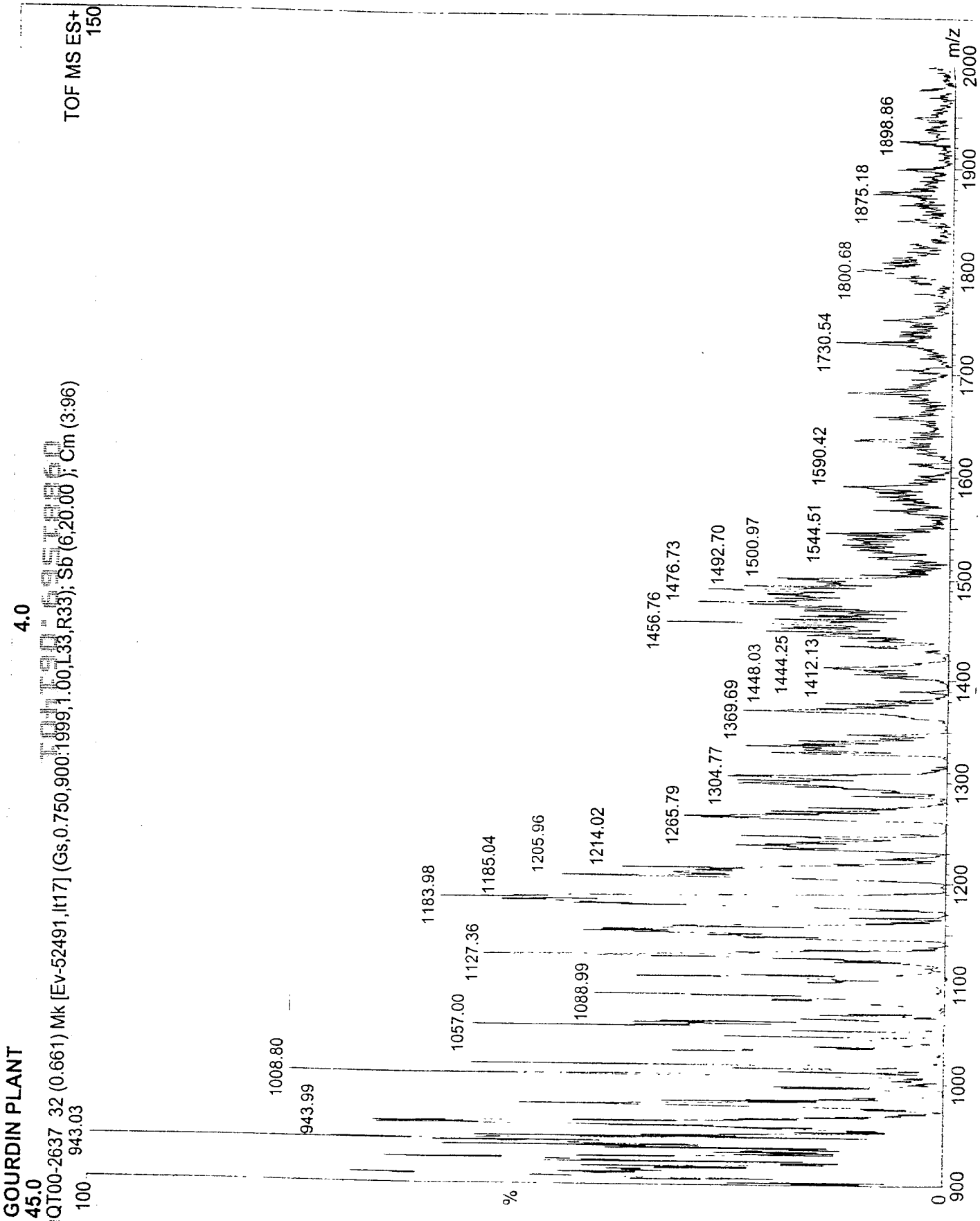

GOURDIN PLANT
45.0
4.0
QT00-2637 32 (0.661) Mk [Ev-52491,It17] (Gs,0.750,900:1999,1.00,L33,R33); Sb (6,20.00); Cm (3:96)
TOF MS ES+
150
100
%
0
943.03
1008.80
943.99
1057.00
1127.36
1183.98
1185.04
1205.96
1214.02
1088.99
1265.79
1304.77
1369.69
1448.03
1444.25
1412.13
1456.76
1476.73
1492.70
1500.97
1544.51
1590.42
1730.54
1800.68
1875.18
1898.86
900
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z

FIG.4(c)

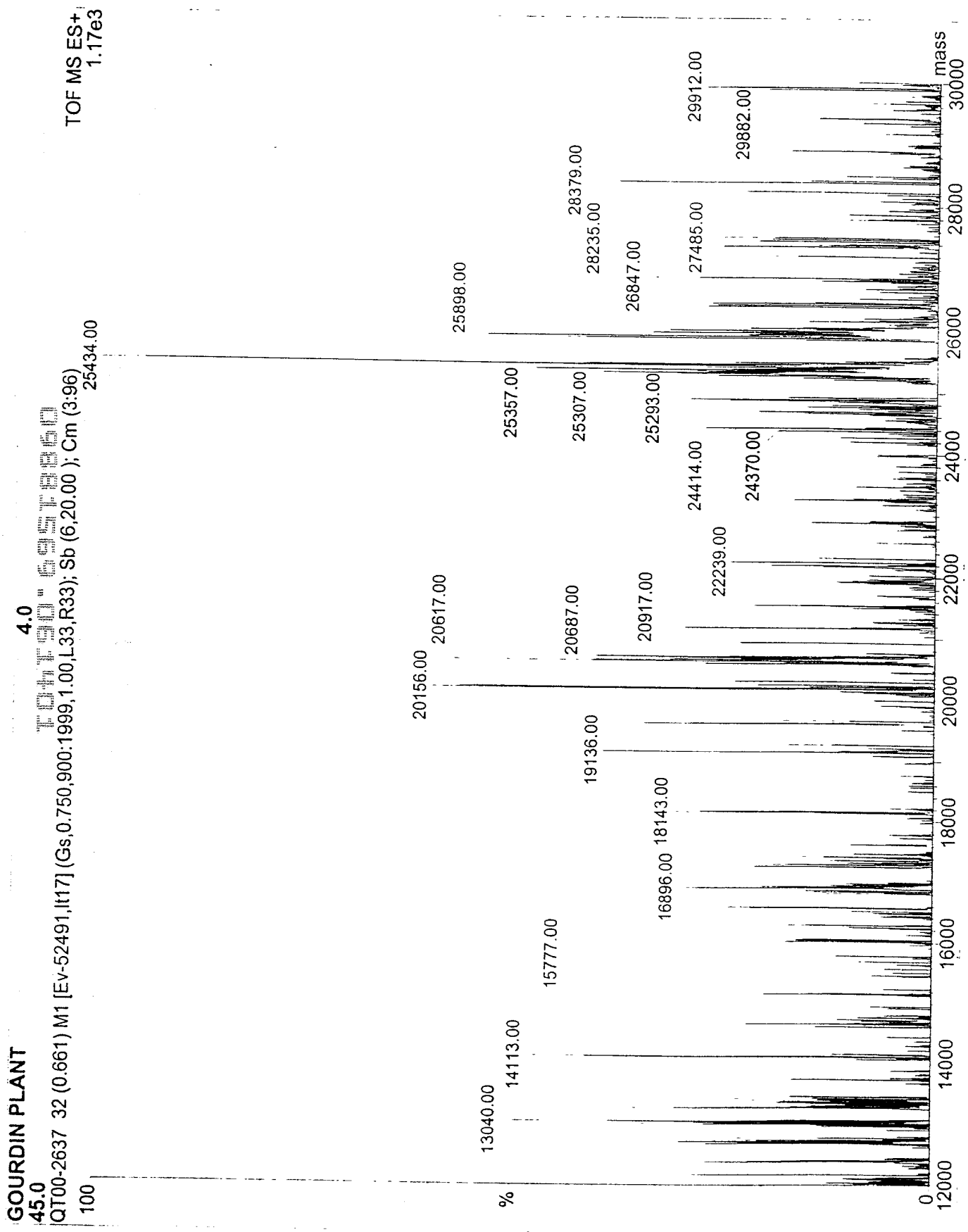

GOURDIN PLANT
45.0
QT00-2637 32 (0.661) M1 [Ev-52491,It17] (Gs,0.750,900:1999,1.00,L33,R33); Sb (6,20.00); Cm (3:96)
100
%
0
4.0
TOF MS ES+
1.17e3
12000
14000
16000
18000
20000
22000
24000
26000
28000
30000
mass
13040.00
14113.00
15777.00
16896.00
18143.00
19136.00
20156.00
20617.00
20687.00
20917.00
22239.00
24370.00
24414.00
25293.00
25307.00
25357.00
25434.00
25898.00
26847.00
28235.00
28379.00
27485.00
29882.00
29912.00

FIG.4(d)

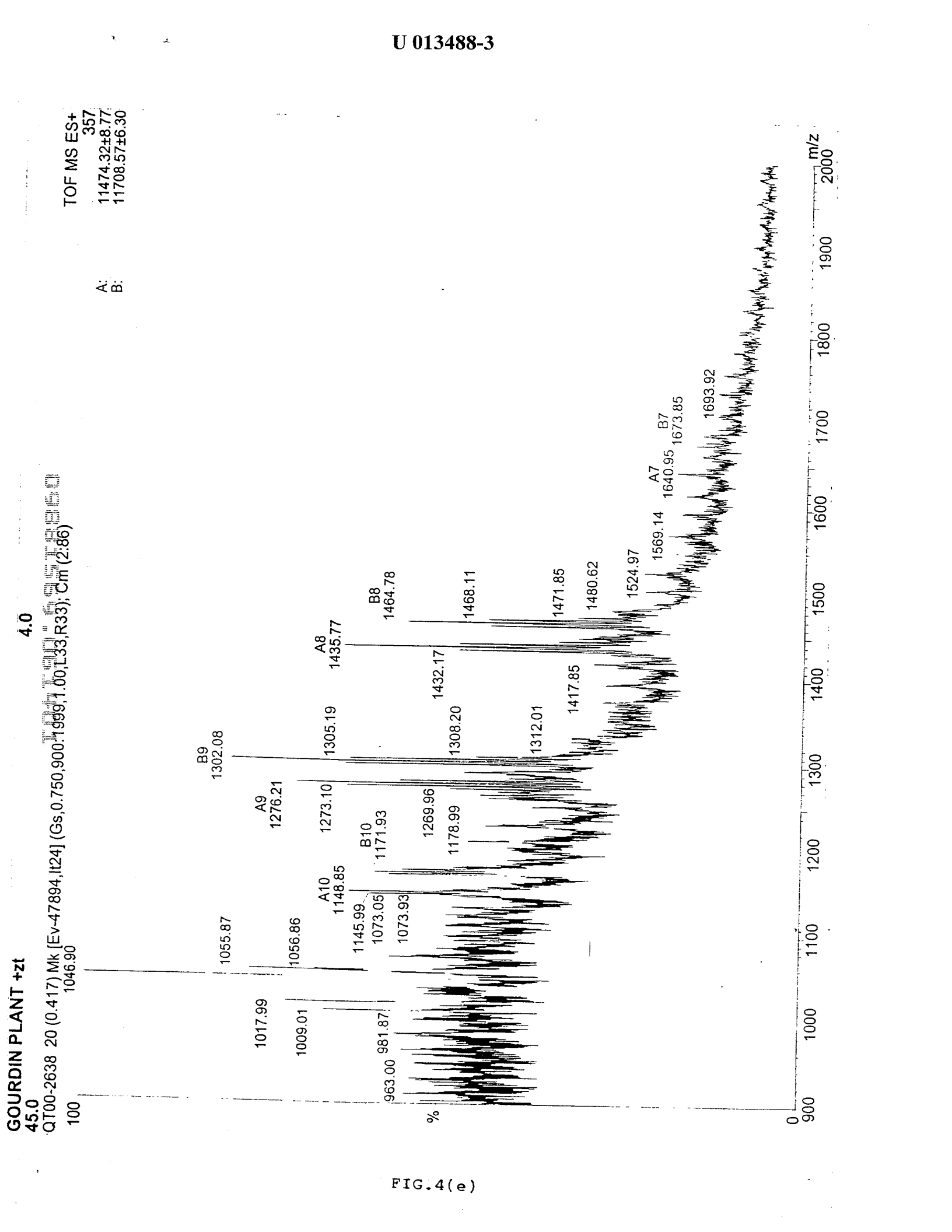
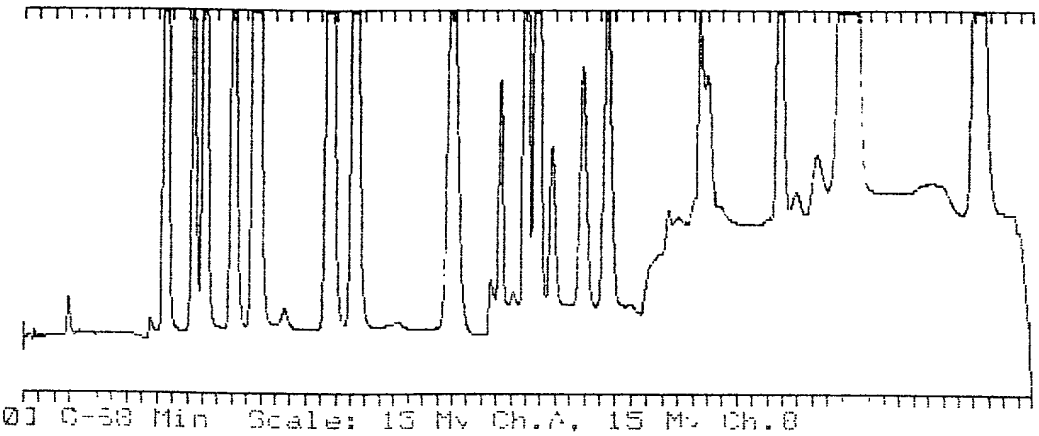

GOURDIN PLANT +zt
45.0
4.0
QT00-2638 20 (0.417) Mk [Ev-47894,It24] (Gs,0.750,900.1999,1.00,L33,R33); Cm (2.86)
TOF MS ES+
357
A: 11474.32±8.77
B: 11708.57±6.30
100
%
0
900
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z
1046.90
1055.87
1017.99
1056.86
1009.01
981.87
963.00
B9
1302.08
A9
1276.21
1273.10
1305.19
A8
1435.77
B8
1464.78
A10
1148.85
1145.99
B10
1171.93
1073.05
1073.93
1269.96
1178.99
1432.17
1308.20
1312.01
1468.11
1471.85
1417.85
1480.62
1524.97
1569.14
A7
1640.95
B7
1673.85
1693.92

FIG.4(e)



[Interface 0] 0-60 Min Scale: 13 Mv Ch.A, 15 Mv Ch.B
amino acid analysi Processed: 11-22-2000 14:26:30, segment 17, cycle 936
RAW DATA SAVED IN FILE K:AAA936.PTS Second Channel Stored in K:BAA936.PTS

EXTERNAL STANDARD TABLE

********** 11-22-2000 14:26:33 Version 4.1 **********
* Sample Name: amino acid analysi Data File: K:AAA936 *
* Date: 11-22-2000 14:26:30 Method: F:REBECKA 11-22-2000 13:54:21 # 457*
* Interface: 0 Cycle#: 936 Operator jmc Channel#: 0 Vial#: N.A. *
* Starting Peak Width: 21 Threshold: .5 Area Threshold: 500 *
****

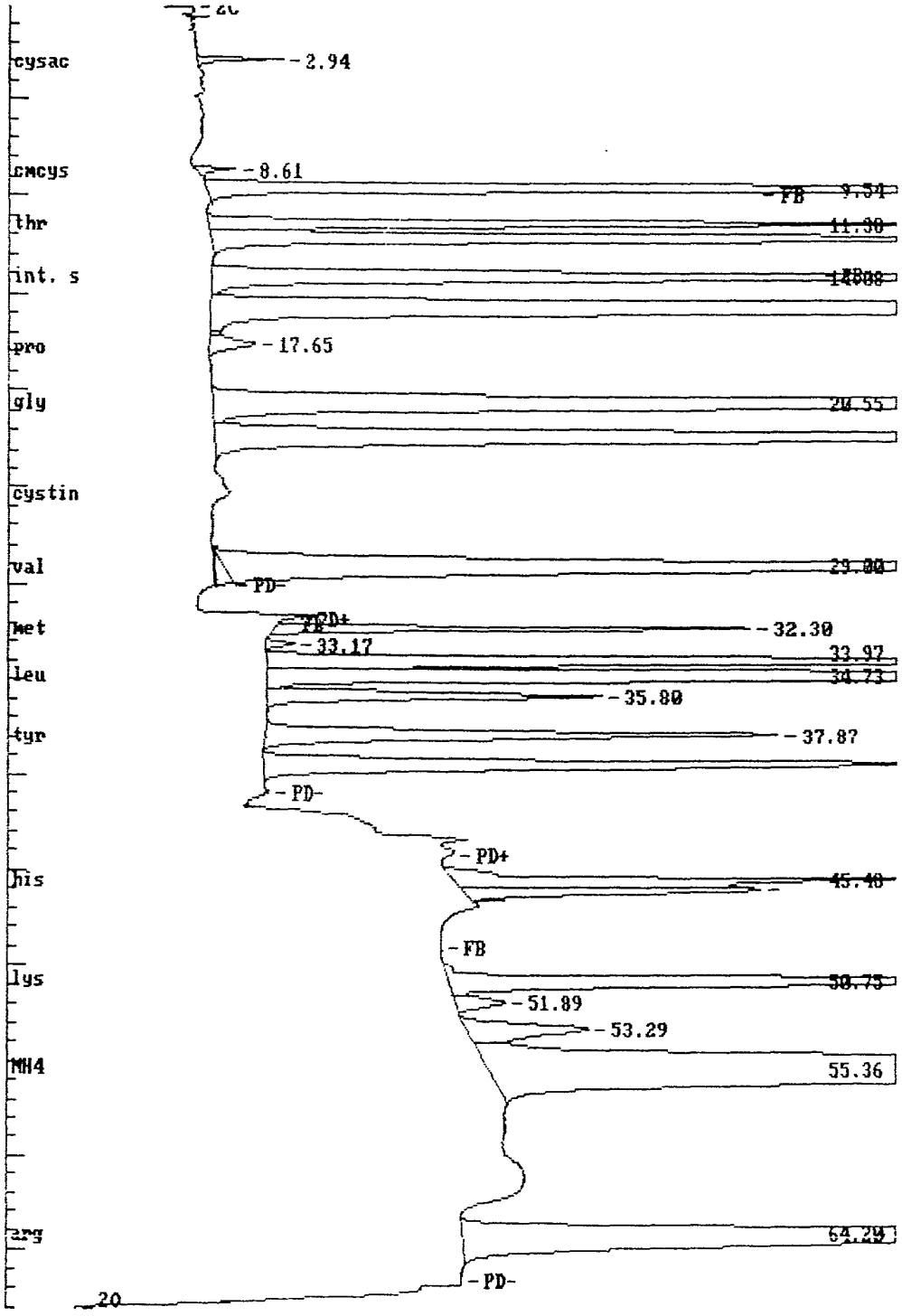
Starting Delay: 0.00 Ending retention time: 68.00
Area reject: 5000 One sample per 2.002 sec.
Amount injected: 1.00 Dilution factor: 1.00
Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/AREA
1	2.936	~~cysac~~	~~0.0711~~	0.1504%	20635	1550	13.4	1	6	-1.592	3.4373E-06
2	8.609	~~cacys~~	~~0.0410~~	0.0866%	9566	696	13.7	1	6	0	4.2818E-06
3	9.543	asx	3.6346	7.6853%	1019304	61489	16.6	1	6	.5811	3.5658E-06
4	11.378	thr	1.1549	2.4420%	314916	15245	20.7	2	6	.1132	3.6674E-06
5	12.112	ser	2.0456	4.3254%	595007	27668	21.5	2	6	0	3.4380E-06
6	14.081	int. std.	1.0397	2.1985%	576309	23599	24.4	2	6	0	1.8041E-06
7	15.649	glx	6.6195	13.9967%	1959672	71617	27.4	2	6	.1667	3.3779E-06
8	17.651	pro ~~+cys~~	(2.1133) ~~2.9045~~	6.1414%	28161	809	34.8	2	6	-.2854	1.0314E-04
9	20.554	gly	3.4509	7.2968%	1098728	36599	30.0	2	9	0	3.1408E-06
10	22.256	ala	2.8168	5.9561%	881412	25276	31.7	2	9	0	3.5148E-06
11	28.996	val	2.616 ~~2.5700~~	5.4358%	703543	16490	42.7	1	9 715 877	0	3.6541E-06
12	32.299	met	0.5625	1.1894%	157161	8772	17.9	1	16	.0101	3.5792E-06
13	33.166		0.0000	0.0000%	10132	523	19.4	1			0.0000E+00
14	33.967	ileu	1.8404	3.8914%	535119	23330	22.9	2	16	-.0931	3.4392E-06
15	34.735	leu	3.1701	6.7031%	953284	38035	25.1	2	16	0	3.3255E-06
16	35.802	nl-std.	0.2739	0.5791%	163238	6196	26.3	2	16	0	1.6777E-06
17	37.871	tyr	1.0645	2.2508%	290327	9412	30.8	1	16	0	3.6666E-06
18	39.473	phe	1.6115	3.4075%	408260	12881	31.7	1	16	0	3.9472E-06
19	45.479	his	(1.211) ~~1.2633~~	2.6711%	203562	8185	24.9	2	16	0	~~6.2059E-06~~
20	46.013		0.0000	0.0000%	154147	5442	28.3	2			0.0000E+00
21	50.751	lys	1.2451	2.6327%	385456	13267	29.1	2	16	0	3.2302E-06
22	51.885	~~trp~~	~~0.1050~~	0.3923%	32441	913	35.5	2	16	0	5.7275E-06
23	53.287		0.0000	0.0000%	102408	2246	45.6	2			0.0000E+00
24	55.355	NH4	6.1666	13.0391%	3568874	61870	57.7	2	16	0	1.7279E-06
25	64.197	arg	3.5602	7.5279%	1016938	22156	45.9	1	16	0	3.5009E-06

TOTAL AMOUNT : 47.2934

FIG.5(a)

Areas, times, and heights stored in: K:AAA936.ATB
Data File = K:AAA936.PTS Printed on 11-22-2000 at 14:27:06
Start time: 0.00 min. Stop time: 68.00 min. Offset: 0 mv.
Full Range: 15 millivolts



EXTERNAL STANDARD TABLE

FIG.5(b)

U 013488-3

******************** 11-22-2000

* Sample Name: amino acid analysi Data File: K:BAA936 *
* Date: 11-22-2000 14:26:30 Method: F:SEBECKA 11-22-2000 13:55:21 # 25 *
* Interface: 0 Cycle#: 936 Operator jm. Channel#: 1 Vial#: N.A. *
* Starting Peak Width: 21 Threshold: .5 Area Threshold: 500 *
****

Starting Delay: 0.00 Ending retention time: 68.00
Area reject: 5000 One sample per 2.002 sec.
Amount injected: 1.00 Dilution factor: 1.00
Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/AREA
1	8.775		0.0000	0.0000%	5113	286	18.0	1			0.0000E+00
2	9.510		0.0000	0.0000%	129394	7707	16.8	1			0.0000E+00
3	11.345		0.0000	0.0000%	24369	1171	21.3	2			0.0000E+00
4	12.079		0.0000	0.0000%	59106	2389	24.7	2			0.0000E+00
5	14.047		0.0000	0.0000%	47121	1978	23.8	1			0.0000E+00
6	15.616	glx	6.2317	74.6757%	375516	13802	27.2	1	7	.2393	1.6595E-05
7	17.651	pro+cys	(2.1133)	25.3244%	199944	6665	30.0	1	7	0	1.0570E-05
8	20.554		0.0000	0.0000%	83682	2753	30.4	1			0.0000E+00
9	22.222		0.0000	0.0000%	67237	2027	33.2	1			0.0000E+00

TOTAL AMOUNT = 8.3451

Areas, times, and heights stored in: K:BAA936.ATB
Data File = K:BAA936.PTS Printed on 11-22-2000 at 14:28:59
Start time: 0.00 min. Stop time: 68.00 min. Offset: -95 mv.
Full Range: 15 millivolts

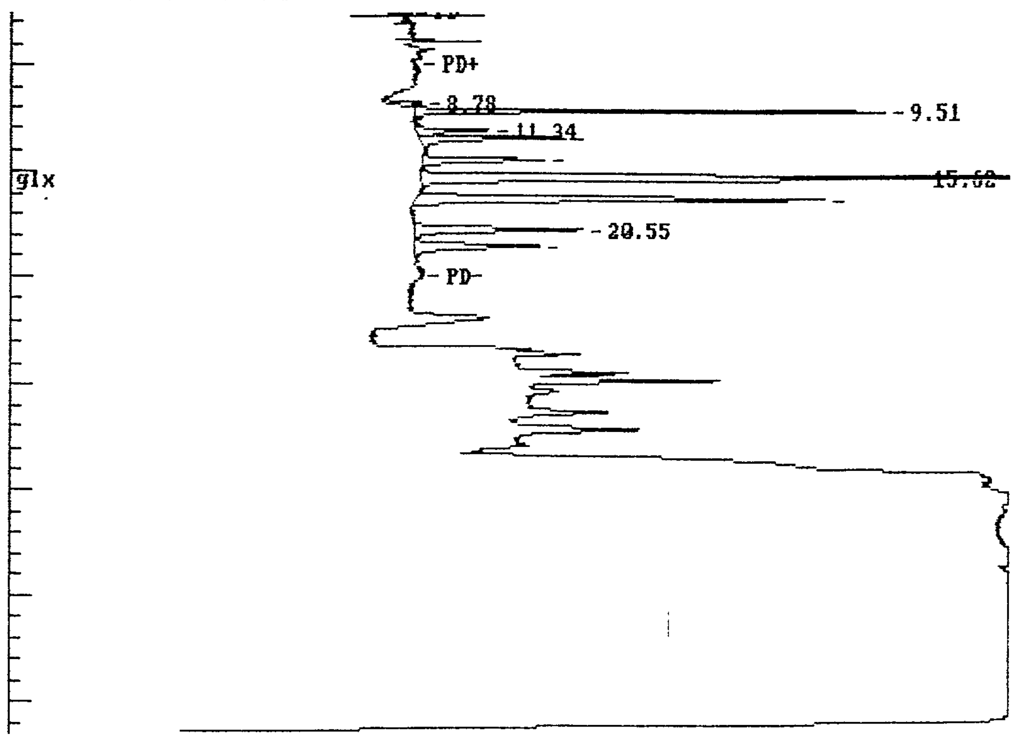


FIG.5(c)